

Section 1

(1)	1	10	20	30	40	50	60	70
gi_3228664_gb_AAC39136.1	(1)	-----	-----	MLSTVFRRTMATGR	-----	HFIAVCQM	TS	DN
gi_3228670_gb_AAC39137.1	(1)	-----	-----	MSTLVNTT	RRSIVIAIHQQLRMSVQKRKD	-----	QSA	TI
gi_3228666_gb_AAC39907.1	(1)	MLGFI	TRPPH	RLSLLCPGLRIPQLSVLCAQPRPRAMAISSS	SC	ELPL	V	AV
gi_3228668_gb_AAC40185.1	(1)	MLGFI	TRPPH	---QLLCTGYRLLRTPVLCTQPRPRMSSSTS	---WEL	PL	V	AV
gi_3242980_gb_AAC40184.1	(1)	MLGFI	TRPPH	---QLLCTGYRLLRIPVLCTQPRPRMSSSTS	---WEL	PL	V	AV
gi_2294001_emb_CAA02248.1	(1)	-----	-----	-----	-----	MKNYP	TV	KV
gi_216934_dbj_BAA01994.1	(1)	-----	-----	-----	-----	MVEY	NT	FK
gi_508735_gb_AAA19627.1	(1)	-----	-----	MSSTEEMSSVKNTTQVIGVDP	SS	TV	RT	IV
gi_508733_gb_AAB60275.1	(1)	-----	-----	-----	-----	MSTSE	NT	PF
gi_1469912_gb_AAB05220.1	(1)	-----	-----	-----	-----	MSTSE	NT	PF
gi_1389699_gb_AAB05221.1	(1)	-----	-----	-----	-----	MSTSE	NT	PF
gi_1181615_dbj_BAA11770.1	(1)	-----	-----	-----	-----	MALV	PT	VP
gi_1171482_dbj_BAA09645.1	(1)	-----	-----	-----	-----	MALV	PT	VP
gi_5953961_gb_AAE06465.1	(1)	-----	-----	-----	-----	XTDY	SG	TF
SEQIDNO:2-09751299	(1)	-----	-----	-----	-----	MSEP	MT	KY
SEQIDNO:4-09751299	(1)	-----	-----	-----	-----	MKEA	IK	VA
Consensus	(1)	-----	-----	-----	-----	S	VRV	AV

Section 2

(71)	71	80	90	100	110	120	130	140
gi_3228664_gb_AAC39136.1	(39)	IERA	GE	KK	CE	W	FL	PE
gi_3228670_gb_AAC39137.1	(57)	VDRA	KS	Q	N	AC	ML	FL
gi_3228666_gb_AAC39907.1	(71)	VR	EA	AR	L	G	AC	IA
gi_3228668_gb_AAC40185.1	(67)	VO	EA	AR	L	G	AC	IA
gi_3242980_gb_AAC40184.1	(67)	VO	EA	AR	L	G	AC	IA
gi_2294001_emb_CAA02248.1	(32)	IA	EA	AS	M	G	AK	VI
gi_216934_dbj_BAA01994.1	(33)	IA	EA	AR	N	G	CE	LV
gi_508735_gb_AAA19627.1	(50)	IV	EA	AS	K	G	AK	LV
gi_508733_gb_AAB60275.1	(43)	IV	EA	AS	K	G	SE	LV
gi_1469912_gb_AAB05220.1	(43)	IV	EA	AT	K	G	SE	LV
gi_1389699_gb_AAB05221.1	(50)	IV	EA	AS	K	G	AE	LV
gi_1181615_dbj_BAA11770.1	(54)	LA	EA	AS	Y	G	AQ	LV
gi_1171482_dbj_BAA09645.1	(54)	LA	EA	AS	Y	G	AQ	LV
gi_5953961_gb_AAE06465.1	(34)	VE	EA	AS	R	A	G	AD
SEQIDNO:2-09751299	(33)	IE	QA	K	Q	D	V	R
SEQIDNO:4-09751299	(30)	ME	EA	AR	N	A	R	L
Consensus	(71)	I	EA	AS	G	A	LV	F

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Section 3

	141	150	160	170	180	190	200	210
gi_3228664_gb_AAC39136.1_	(141)	WLSLGGIHHKDPDS--AAHPWNHHT	IDS DGVTRAEYVKNKHLHFDLE	IIPGKVR	MESEFSKAGTEMIPVVD			
gi_3228670_gb_AAC39137.1_	(91)	WISLGGVHERN-----DQKIFNAHVL	LNEKGEAAVYRKLHMFDMVT	TK-EVRLRES	DTVTPGYCLERPVS			
gi_3228666_gb_AAC39907.1_	(109)	WLSLGGFHERGQDWEQTKFYNCHVL	LNSKGANVATYRKTTHLCDVEI	PGQPMCES	NSTMPGPSLES	PVS		
gi_3228668_gb_AAC40185.1_	(123)	WLSLGGFHERGQDWEQNKQIYNCHVL	LNSKGSVVASVYRKTTHLCDVEI	PGQPMRES	NYTKPGGTLEPPVK			
gi_3242980_gb_AAC40184.1_	(119)	WLSLGGFHERGQDWEQNKQIYNCHVL	LNSKGSVVASVYRKTTHLCDVEI	PGQPMRES	NYTKPGGTLEPPVK			
gi_2294001_emb_CAA02248.1_	(119)	WLSLGGFHERGQDWEQNKQIYNCHVL	LNSKGSVVASVYRKTTHLCDVEI	PGQPMRES	NYTKPGGTLEPPVK			
gi_216934_dbj_BAA01994.1_	(97)	XVCMVSSEKDN-----ASLYLTQLWF	DPNGNEIGKHKRKFKPTSSERA	VWGDG	DGGS-----MA	BVFK		
gi_508735_gb_AAA19627.1_	(99)	AVVVGISERDG-----GSLYMTQLVI	DADGQLVARRRKLPKPTTHVERS	VYGE	NGS-----D	ISVYD		
gi_508732_gb_AAB60275.1_	(120)	HLVMGATIEKDG-----YTLYCTALFF	ESPOGQFLGKHKRKMPTSLERC	IWQGD	DGGS-----T	IPVYD		
gi_1469912_gb_AAB05220.1_	(113)	YLVMGATIEKDG-----YTLYCTALFF	ESPOGQFLGKHKRKMPTSLERC	IWQGD	DGGS-----T	IPVYD		
gi_1389699_gb_AAB05221.1_	(113)	YLVMGATIEKDG-----YTLYCTALFF	ESPOGQFLGKHKRKMPTSLERC	IWQGD	DGGS-----T	IPVYD		
gi_1181615_dbj_BAA11770.1_	(120)	YLVMGATIEKDG-----YTLYCTALFF	ESPOGQFLGKHKRKMPTSLERC	IWQGD	DGGS-----T	IPVYD		
gi_1171482_dbj_BAA09645.1_	(124)	YLVMGATIEKDG-----YTLYCTALFF	ESPOGQFLGKHKRKMPTSLERC	IWQGD	DGGS-----T	IPVYD		
gi_5953961_gb_AAE06465.1_	(124)	YLVMGATIEKDG-----YTLYCTALFF	ESPOGQFLGKHKRKMPTSLERC	IWQGD	DGGS-----T	IPVYD		
SEQIDNO:2-09751299	(99)	ATMGFSERGH-----GSLYMGQAI	EPDGDLEAARRKLPKPTTHVERS	TFEGE	DGGS-----D	LVMDQ		
SEQIDNO:4-09751299	(98)	HVAGYSERAG-----GSLYMGQAI	EPDGDLEAARRKLPKPTTHVERS	TFEGE	DGGS-----D	LVMDQ		
	(95)	MVTLGMSERVG-----GLYISQWFIG	NDTLCARERKLPKPTTHVERS	TFEGE	DGGS-----D	LVMDQ		
Consensus (141)		YLVMGATIEKDG	TLY T LLF QG LLGKHKRKL PT LER IWG GDGS			IPVYD		

Section 4

	211	220	230	240	250	260	270	280
gi_3228664_gb_AAC39136.1_	(211)	TPIGRLGSLCTCYDVRF	ELSLWNRKRGAQILSFPSAFT	-----LNTG	LAHMETL	LARARAE		
gi_3228670_gb_AAC39137.1_	(159)	TPVGLGLOFCYDLRFAEPAVL	ERKLKANLLTYPSAFT	-----YATG	KAHMETL	LARARAE		
gi_3228666_gb_AAC39907.1_	(173)	TPAGKTLGAVCYDMRFF	ELSLSLAQAAGAILTYPSAFT	-----SITG	PAHMETL	LARARAE		
gi_3228668_gb_AAC40185.1_	(193)	TPAGKTLGAVCYDMRFF	ELSLSLAQAAGAILTYPSAFT	-----SVTG	PAHMETL	LARARAE		
gi_3242980_gb_AAC40184.1_	(189)	TPAGKTLGAVCYDMRFF	ELSLSLAQAAGAILTYPSAFT	-----SVTG	PAHMETL	LARARAE		
gi_2294001_emb_CAA02248.1_	(189)	TPAGKTLGAVCYDMRFF	ELSLSLAQAAGAILTYPSAFT	-----SVTG	PAHMETL	LARARAE		
gi_216934_dbj_BAA01994.1_	(153)	TEYGNELGGLQCWEHALP	ENIAAMGSLNEQVHVASWPAFV	PKGAVSSRVSSSVCA	STNAMHQIISQFYA	IS		
gi_508735_gb_AAA19627.1_	(155)	MPFARLGALNCWEHFQTL	TKVAMYSMHEQVHVASWPGMSLY	-----QPEVPAF	GVDAQLT	ATRM	YALE	
gi_508733_gb_AAB60275.1_	(176)	TPIGKLGAAICWENRMPL	YRTALYAKGIELYCAPTADY	-----SLEW	QASMI	HIHIAVE		
gi_1469912_gb_AAB05220.1_	(169)	TPIGKLGAAICWENRMPL	YRTALYAKGIELYCAPTADY	-----SLEW	QASMI	HIHIAVE		
gi_1389699_gb_AAB05221.1_	(169)	TPIGKLGAAICWENRMPL	YRTALYAKGIELYCAPTADY	-----SLEW	QASMI	HIHIAVE		
gi_1181615_dbj_BAA11770.1_	(176)	TPIGKLGAAICWENRMPL	YRTALYAKGIELYCAPTADY	-----SLEW	QASMI	HIHIAVE		
gi_1171482_dbj_BAA09645.1_	(180)	TPIGKLGAAICWENRMPL	YRTALYAKGIELYCAPTADY	-----SLEW	QASMI	HIHIAVE		
gi_5953961_gb_AAE06465.1_	(180)	TPIGKLGAAICWENRMPL	YRTALYAKGIELYCAPTADY	-----SLEW	QASMI	HIHIAVE		
SEQIDNO:2-09751299	(155)	TSLGRVGLCCWEHLQPL	TKVAMYSQHEQIHIAWPSFSIF	-----PGAVYAL	GPEVNTA	AASQYAVE		
SEQIDNO:4-09751299	(154)	TAIGRLGALCCWEHIQPL	SKVAMAYADEQVHVASWPSFSLY	-----RGMAYAL	GPEVNTA	AASQYAVE		
SEQIDNO:4-09751299	(151)	TSVGRIGLCCWEHLQPL	TKVAMYSQHEQIHIAWPSFSLY	-----PNAAKAL	GPDVNV	AASRIYAVE		
Consensus (211)		TPIGKLGAAICWE R PL R ALYA G EIY APTA				G W ASM AIE		

350

	(281)	281	290	300	310	320	330	340	350				
gi_3228664_gb_AAC39136.1_	(215)	NQCYVAAQAQTGAHN-----PK---	RQSYGHSNVDPWGAVVAQCSE--VDMCFAE										
gi_3228670_gb_AAC39137.1_	(229)	TQCFVAAQAQIGWHN-----QK---	RQSWGHSNIVSPWGNVLADCSEQE-LDIGTAE										
gi_3228666_gb_AAC3907.1_	(249)	TQCYVAAQAQCGRHH-----EK---	RASYGHSNVDPWGTVAARCSEG--PGLCLAR										
gi_3228668_gb_AAC40185.1_	(245)	SOQYVIAAQAQCGRHH-----ET---	RASYGHSNVDPWGTVAARCSEG--PGLCLAR										
gi_3242980_gb_AAC40184.1_	(245)	SOQYVIAAQAQCGRHH-----ET---	RASYGHSNVDPWGTVAARCSEG--PGLCLAR										
gi_2294001_emb_CAA02248.1_	(223)	NOYVIMSTNLVG-----QDMIDMIGKDEFSKNFLPLGSGNTAIIISNTGEILASIPQDA-EGIAVAE											
gi_216934_dbj_BAA01994.1_	(218)	GOTFVVCCTQVVT-----PEAHEFFCNDDEQRKLI	GRGGGFARIICPDGRDLATPLAEDEEGILYAD										
gi_508735_gb_AAA19627.1_	(228)	GGCFVLSAHQFCKRREFPEHPDYLFNNDIVDTKEHDPTVSGGG--SVIISPLGKVLAGPNYFS-EGLVTA											
gi_508733_gb_AAB60275.1_	(221)	GGCFVLSACQFCLRKDEPDHPDYLFFTDWYDDEPDDSIVSQGG--SVIISPLGQVLAGPNFES-EGELITAD											
gi_1469912_gb_AAB05220.1_	(221)	GGCFVLSACQFCLRKDEPDHPDYLFFTDWYDDEPDDSIVSQGG--SVIISPLGQVLAGPNFES-EGELITAD											
gi_1389899_gb_AAB05221.1_	(228)	GGCFVLSACQFQCRKHFPDHPDYLFFTDWYDDEPDDSIVSQGG--SVIISPLGQVLAGPNFES-EGELITAD											
gi_1181615_dbj_BAA11770.1_	(232)	GGCFVLSANQFCRRKDYPPPEYVFSG-TEEDLTPDSDIVCAGG--SVIISPSGAVLAGPNYEG-FALISAD											
gi_1171482_dbj_BAA09645.1_	(232)	GGCFVLSANQFCRRKDYPPPEYVFSGTEEDLTPDSDIVCAGG--SVIISPSGAVLAGPNYVG-FALISAD											
gi_5953961_gb_AAE06465.1_	(218)	GOTXVLAFCVIG-----DAGWEAFADTEEKRLTHKGGGYARIYCPDGRSLAEPLAPNDEEGILYAD											
SEQIDNO:2-09751299	(217)	GGCYVLAFCATVS-----PENIKVLVDTDDKEMFLKAGGGFAMIFGPDGRAFLAEPLPETEEGLLVAD											
SEQIDNO:4-09751299	(214)	GOCFVLAFCALVS-----QSMIDMLCTDDEKHALLLAGGGHSRIIGPDGDDLVAFLAENEEGILYAN											
Consensus (281)		GQCFVLAQ	L	D	E	IV	AGGG	SMIISP	GVLA	P	E	EGLI	AD

Section 6

	(351)	351	360	370	380	390	400	410	420
gi_3228664_gb_AAC39136.1_	(262)	TDLSYVDTLREMQPVFSHRRSDLYTLHINEKSS--TGGKFAFARNIPADHIFYSTPHSFVFNLPVTD							
gi_3228670_gb_AAC39137.1_	(277)	VDLSVLQSLYQTMPCFEHRRNDIYALTAYNLSRKEPTQDRPFATNIVDKRTIFYESEHCFAFTNLRVCVK							
gi_3228666_gb_AAC39907.1_	(296)	IDLNYLRQLRRHLVPVQHRRPDLYGNLGHPLS----							
gi_3228668_gb_AAC40185.1_	(292)	IDLHFLQQMRQHLPLVFQHRRPDLYGS LGHPLS----							
gi_3242980_gb_AAC40184.1_	(292)	IDLHFLQQMRQHLPLVFQHRRPDLYGS LGHPLS----							
gi_2294001_emb_CAA02248.1_	(284)	IDLNQIIYGGKWLDPAGHYSTPGFSLSTFDQSEHVVPVKKIGEQTNHFI SYEDLHEDKMDMLTIPPRRVAT							
gi_216934_dbj_BAA01994.1_	(280)	IDLSAITLAKQAADPVGHYSRRPDVLS LNFNQRHTTTPVNTAISTIHATHTLVPQSGALDGVRELNGADEQR							
gi_508735_gb_AAA19627.1_	(295)	LDLGDIAAKLYFDVGHYSKRPDIENLTWNEHPKKPVTFMTKVEKAEDSNK----							
gi_508733_gb_AAB60275.1_	(288)	LDLGDVARAKLYFDSVGHYSRRPDVHLTWNEHPKKPVTFISKVEKAEDDSNK----							
gi_1469912_gb_AAB05220.1_	(288)	LDLGDVARAKLYFDSVGHYSRRPDVHLTWNEHPKKPVTFISKVEKAEDDSNK----							
gi_1389699_gb_AAB05221.1_	(295)	LDLGDIAAKLYFDSVGHYSRRPDVHLTWNEHPKKPVTFISKVEKAEDDSNK----							
gi_1181615_dbj_BAA11770.1_	(298)	LDLGEIARAKFDFDVGHYARPEVLSIWRDHAVSPVSFTSTSSKAES-SPK----							
gi_1171482_dbj_BAA09645.1_	(299)	LDLGEIARAKFDFDVGHYARPEVLSIWRDHAVSPVSFTSTSSKAES-SPK----							
gi_5953961_gb_AAE06465.1_	(280)	IDLSAILAAKNPADPVGHYSRRPDVLR LGFNKAPQPKVNI LGTEPSRTTSTQCRPTTIRRSWRFPE----							
SEQIDNO:2-09751299	(279)	IDLGMIALAKAAADPAGHYSRRPDVTRL LDRRPAQRVVT L DAAFE PQNEDKGDAPALRVVAESAAAAQ----							
SEQIDNO:4-09751299	(276)	LDPGVRIILAKMAADPAGHYSRRPDITRL LIDRSPKLPVVEIEGDLRPYALGKASETGAQLEEI----							
Consensus (351)		IDLG I AK D VGHYSRRPDV L V PV I							

## Section 7

	(421)	421	430	440	450	460	470	480	490
gi_3228664_gb_AAC39136.1_	(330)	GHVLVSPKRVVPRRLTDLTDAETADLFIVAKKVQAMLEKHHNVTS	TTICVQDGGKDAAGQTVPHVHIHILPRR						
gi_3228670_gb_AAC39137.1_	(347)	GHVLVSTKRVTPLRCGLDCAEMADMFTTVC	LVQRLLLEKIYQTTSATVTVQDGAQAGQTVPHVHFHIMPRR						
gi_3228666_gb_AAC39907.1_	(328)								
gi_3228668_gb_AAC40185.1_	(324)								
gi_3242980_gb_AAC40184.1_	(324)								
gi_2294001_emb_CAA02248.1_	(354)	A							
gi_216934_dbj_BAA01994.1_	(350)	ALPSTHSDTDRATASI							
gi_508735_gb_AAA19627.1_	(347)								
gi_508733_gb_AAB60275.1_	(340)								
gi_1469912_gb_AAB05220.1_	(340)								
gi_1389699_gb_AAB05221.1_	(347)								
gi_1181615_dbj_BAA11770.1_	(349)								
gi_1171482_dbj_BAA09645.1_	(350)								
gi_5953961_gb_AAE06465.1_	(345)								
SEQIDNO:2-09751299	(347)								
SEQIDNO:4-09751299	(338)								
Consensus (421)									

## Section 8

	(491)	491	500	510	520	535
gi_3228664_gb_AAC39136.1_	(400)	AGDFGDNEIYQKSLASHDKPERKPRSNEQMAEEAVVYRNL	---			
gi_3228670_gb_AAC39137.1_	(417)	LGDFGHNDQIYVKLDERAE-EKPPRTIEERIEEAQIYRKFLTDIS				
gi_3228666_gb_AAC39907.1_	(328)					
gi_3228668_gb_AAC40185.1_	(324)					
gi_3242980_gb_AAC40184.1_	(324)					
gi_2294001_emb_CAA02248.1_	(355)					
gi_216934_dbj_BAA01994.1_	(367)					
gi_508735_gb_AAA19627.1_	(347)					
gi_508733_gb_AAB60275.1_	(340)					
gi_1469912_gb_AAB05220.1_	(340)					
gi_1389699_gb_AAB05221.1_	(347)					
gi_1181615_dbj_BAA11770.1_	(349)					
gi_1171482_dbj_BAA09645.1_	(350)					
gi_5953961_gb_AAE06465.1_	(345)					
SEQIDNO:2-09751299	(347)					
SEQIDNO:4-09751299	(338)					
Consensus (491)						